

SEQUENCE LISTING

<110> BROWN, JAMES R.
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<120> Methods Using Mechanisms of Action of
AroA

<130> GM50053

<140> To Be Assigned

<141> 2001-11-05

<150> PCT/US00/12251

<151> 2000-05-04

<150> 60/133,070

<151> 1999-05-07

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1284

<212> DNA

<213> Streptococcus pneumonie

<400> 1

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gatattctgc gaggtgaaga cgttctttcg accatgcagg tttttcgtga ccttggtgtt 180
gaaattgagg ataaagatgg gggtattacc gttcaagggt taggcatggc tggcttaaaa 240
gcgccgcaaa atgcccttaa tatgggaaat tctggcacct cgattcgcct gatttcaggt 300

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cctatggacc gtgtgacctt tccactgaaa aaaatgggag tcagcatctc agggcaaaact 420
gaacgagact tgcctccctt tcgcttaaaa gggacgaaaa acctaagacc tattcattat 480
gagttgccaa ttgcctctgc ccaagtcaag tcagccttga tgtttgcagc cttacaagct 540
aagggggagt cagttattat cgaaaaagag tacaccgta atcatactga agatatgttg 600
caacaatttg gtggtcattt aagtgtggat ggtaagaaaa tcacagtcca agggccacaa 660
aaattgacag gacagaaggt ggtcgtacca ggagatattt ccagtgcagc cttttggtta 720
gtcgcagggt tgattgctcc aaattctcgt ctagtgcctgc agaattgtggg gataaacgaa 780
actcgcaccg gtattattga tgtcattcgt gccatgggtg gaaaattgga aataactgaa 840
atcgatccag tcgctaaatc tgcaaccttg attgttgagt cttctgactt gaaaggaaca 900
gagatttggt ggcctttgat tccagtttg attgatgaat tgccattat tgcctactt 960
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acggcagatg ggatgattat caaaggaaaa tcagctcttc acggtgctag agtcaatacg 1140
tttggtgacc accgtatcgg catgatgaca gctatcgcag cctattggt tgcagatgga 1200
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1284

<210> 2

<211> 427

<212> PRT

<213> Streptococcus pneumoniae

<400> 2

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Ala Glu Gly Glu Thr Lys Val Tyr Asp Ile Leu Arg Gly Glu Asp Val
      35             40             45
Leu Ser Thr Met Gln Val Phe Arg Asp Leu Gly Val Glu Ile Glu Asp
      50             55             60
Lys Asp Gly Val Ile Thr Val Gln Gly Val Gly Met Ala Gly Leu Lys
      65             70             75             80
Ala Pro Gln Asn Ala Leu Asn Met Gly Asn Ser Gly Thr Ser Ile Arg
      85             90             95
Leu Ile Ser Gly Val Leu Ala Gly Ala Asp Phe Glu Val Glu Met Phe
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Gly Asp Asp Ser Leu Ser Lys Arg Pro Met Asp Arg Val Thr Leu Pro
      115            120            125

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Glu	Leu	Pro	Ile	Ala	Ser	Ala	Gln	Val	Lys	Ser	Ala	Leu	Met	Phe	Ala	165	170	175
Ala	Leu	Gln	Ala	Lys	Gly	Glu	Ser	Val	Ile	Ile	Glu	Lys	Glu	Tyr	Thr	180	185	190
Arg	Asn	His	Thr	Glu	Asp	Met	Leu	Gln	Gln	Phe	Gly	Gly	His	Leu	Ser	195	200	205
Val	Asp	Gly	Lys	Lys	Ile	Thr	Val	Gln	Gly	Pro	Gln	Lys	Leu	Thr	Gly	210	215	220
Gln	Lys	Val	Val	Val	Pro	Gly	Asp	Ile	Ser	Ser	Ala	Ala	Phe	Trp	Leu	225	230	235
Val	Ala	Gly	Leu	Ile	Ala	Pro	Asn	Ser	Arg	Leu	Val	Leu	Gln	Asn	Val	245	250	255
Gly	Ile	Asn	Glu	Thr	Arg	Thr	Gly	Ile	Ile	Asp	Val	Ile	Arg	Ala	Met	260	265	270
Gly	Gly	Lys	Leu	Glu	Ile	Thr	Glu	Ile	Asp	Pro	Val	Ala	Lys	Ser	Ala	275	280	285
Thr	Leu	Ile	Val	Glu	Ser	Ser	Asp	Leu	Lys	Gly	Thr	Glu	Ile	Cys	Gly	290	295	300
Ala	Leu	Ile	Pro	Arg	Leu	Ile	Asp	Glu	Leu	Pro	Ile	Ile	Ala	Leu	Leu	305	310	315
Ala	Thr	Gln	Ala	Gln	Gly	Val	Thr	Val	Ile	Lys	Asp	Ala	Glu	Glu	Leu	325	330	335
Lys	Val	Lys	Glu	Thr	Asp	Arg	Ile	Gln	Val	Val	Ala	Asp	Ala	Leu	Asn	340	345	350
Ser	Met	Gly	Ala	Asp	Ile	Thr	Pro	Thr	Ala	Asp	Gly	Met	Ile	Ile	Lys	355	360	365
Gly	Lys	Ser	Ala	Leu	His	Gly	Ala	Arg	Val	Asn	Thr	Phe	Gly	Asp	His	370	375	380
Arg	Ile	Gly	Met	Met	Thr	Ala	Ile	Ala	Ala	Leu	Leu	Val	Ala	Asp	Gly	385	390	395
Glu	Val	Glu	Leu	Asp	Arg	Ala	Glu	Ala	Ile	Asn	Thr	Ser	Tyr	Pro	Ser	405	410	415
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<210> 3
<211> 1245
<212> DNA
<213> Streptococcus pneumoniae

<220>
<221> unsure
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<223> (492) (493) (494) (495) (496) (497) (498) (499)
<224> Where n can be represented by a, c, t, or g

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caggtttttc gtgaccttgg tgttgaaatt gaggataaag atgggggttat taocgttcaa 180
ggtgtaggca tgggtggcctt aaaagcgccg caaaatgccc ttaatatggg aaattctggc 240
acctcgattc gcttgatttc aggtgtcctt gctgggtgcag atttcgaagt agagatgttt 300
ggagatgata gtctttccaa acgtcctatg gaccgtgtga ccttccact gaaaaaaatg 360
ggcgtcagca tctcagggca aactgaacga gacttgcttc ccttctgctt taaaagggac 420
gaaaaaccta agacctattc attatgagtt gccaatggc tetgcccag tcaagtcagc 480
cnnnnnnnnn nnnnnnnnnn taagggggag tcagttatta tcgaaaaaga gtacaccctg 540
aatcatactg aagatatgtt gcaacaattt ggtgggtcatt taagtgtgga tggtaagaaa 600
atcacagtcc aagggccaca aaaattgaca ggacagaagg tggtcgtacc aggagatatt 660
tccagtgcag ccttttggtt agtcgcaggt ttgattgctc caaattctcg tctagtgtcg 720
cagaatgrgg ggataaacga aactgcacc ggtattattg atgtcattcg tgccatgggt 780
ggaaaattgg aaataactga aatcgatcca gtcgctaaat ctgcaacctt gattgttgag 840
tcttctgact tgaaaggaac agagatttgt ggcgctttga ttccacgttt gattgatgaa 900
ttgcctatta ttgcctact tgcgacccaa gcccaagggtg taacagttat caaggatgct 960
gaggagctca aggtcaagga aacagaccgt attcaggttg tggcagacgc cttaaatagt 1020
atggggagcag atattactcc tacggcagat gggatgatta tcaaaggaaa atcagctctt 1080
cacggtgcta gagtcaatac gtttggtgac caccgtatcg gcattgatgac agctatcgca 1140
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<210> 4
<211> 415
<212> PRT
<213> Streptococcus pneumoniae

<220>

<221> unsure

<222> (149) ((161) (162) (163) (164) (165) (166) (167) (168))

<223> Where Xaa can be represented by any one of the twenty naturally

<223> occurring proteins

<400> 4

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			20					25					30		
Gly	Glu	His	Val	Leu	Ser	Thr	Met	Gln	Val	Phe	Arg	Asp	Leu	Gly	Val
		35					40					45			
Glu	Ile	Glu	Asp	Lys	Asp	Gly	Val	Ile	Thr	Val	Gln	Gly	Val	Gly	Met
	50					55					60				
Ala	Gly	Leu	Lys	Ala	Pro	Gln	Asn	Ala	Leu	Asn	Met	Gly	Asn	Ser	Gly
65					70					75					80
Thr	Ser	Ile	Arg	Leu	Ile	Ser	Gly	Val	Leu	Ala	Gly	Ala	Asp	Phe	Glu
			85					90					95		
Val	Glu	Met	Phe	Gly	Asp	Asp	Ser	Leu	Ser	Lys	Arg	Pro	Met	Asp	Arg
			100					105					110		
Val	Thr	Leu	Pro	Leu	Lys	Lys	Met	Gly	Val	Ser	Ile	Ser	Gly	Gln	Thr
		115					120						125		
Glu	Arg	Asp	Leu	Pro	Pro	Leu	Arg	Phe	Lys	Arg	Asp	Glu	Lys	Pro	Lys
	130					135					140				
Thr	Tyr	Ser	Leu	Xaa	Val	Ala	Asn	Cys	Leu	Cys	Pro	Ser	Gln	Val	Ser
145					150					155					160
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Gly	Glu	Ser	Val	Ile	Ile	Glu
				165					170				175		
Lys	Glu	Tyr	Thr	Arg	Asn	His	Thr	Glu	Asp	Met	Leu	Gln	Gln	Phe	Gly
			180					185					190		
Gly	His	Leu	Ser	Val	Asp	Gly	Lys	Lys	Ile	Thr	Val	Gln	Gly	Pro	Gln
	195					200						205			
Lys	Leu	Thr	Gly	Gln	Lys	Val	Val	Val	Pro	Gly	Asp	Ile	Ser	Ser	Ala
	210					215					220				
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225					230					235					240
Leu	Gln	Asn	Val	Gly	Ile	Asn	Glu	Thr	Arg	Thr	Gly	Ile	Ile	Asp	Val
			245					250					255		
Ile	Arg	Ala	Met	Gly	Gly	Lys	Leu	Glu	Ile	Thr	Glu	Ile	Asp	Pro	Val
			260					265					270		

Ala	Lys	Ser	Ala	Thr	Leu	Ile	Val	Glu	Ser	Ser	Asp	Leu	Lys	Gly	Thr	275	280	285
Glu	Ile	Cys	Gly	Ala	Leu	Ile	Pro	Arg	Leu	Ile	Asp	Glu	Leu	Pro	Ile	290	295	300
Ile	Ala	Leu	Leu	Ala	Thr	Gln	Ala	Gln	Gly	Val	Thr	Val	Ile	Lys	Asp	305	310	315
Ala	Glu	Glu	Leu	Lys	Val	Lys	Glu	Thr	Asp	Arg	Ile	Gln	Val	Val	Ala	325	330	335
Asp	Ala	Leu	Asn	Ser	Met	Gly	Ala	Asp	Ile	Thr	Pro	Thr	Ala	Asp	Gly	340	345	350
Met	Ile	Ile	Lys	Gly	Lys	Ser	Ala	Leu	His	Gly	Ala	Arg	Val	Asn	Thr	355	360	365
Phe	Gly	Asp	His	Arg	Ile	Gly	Met	Met	Thr	Ala	Ile	Ala	Ala	Leu	Leu	370	375	380
Val	Ala	Asp	Gly	Glu	Val	Glu	Leu	Asp	Arg	Ala	Glu	Ala	Ile	Asn	Thr	385	390	395
Ser	Tyr	Pro	Ser	Phe	Phe	Asp	Asp	Leu	Glu	Ser	Leu	Ile	His	Gly		405	410	415